



AGGAGCAGTTACGGTCTGTGTCCAGTGACTGACTCTACCCAGAAT	+-----+-----+-----+-----+-----+-----+-----+	181	240
TCCTCGTCATGCCAGACACAGGGTACATCTACTGACTGACATGAGGATGGTCTTA	+-----+-----+-----+-----+-----+-----+-----+		
		E Q L R S V S S V D E L M T V L Y P E Y -	

CCCCAACCTCAACTCAAGGACAGAAAGAGACTATAAAAATTGGCTSCAGCACATTATAATACAG

MATCH WITH FIG. 1B

FIG. 1A



MATCH WITH FIG. 1A

301 +-----+
 GGTGGAGTTGAGTCCCTGTCTTGATATTAAACGACGTCGTGTAATAATTATGTC
 N L N S R T E E T I K F A A H Y N T E -
 AGATCTTGAAGTATTGATAATGAGTGGAGAAAGACTCAATGCCATGGGAGGGTGT
 361 +-----+
 TCTAGAACTTTCTATAACTATTACTCACCTCTTGAGTTACGGTACGGTGCCTCCACA
 I L K S I D N E W R K T Q C M P R E V C -
 GTATAGATGTGGGAAGGAGTTGGAGTCGGACAAACACCTTCTTAAACCTCCATGTG
 421 +-----+
 CATATCTACACCCCTCCTCAACCTCAGGGCTGTGTTGTGGAAGAAATTGGAGGTACAC
 I D V G K E F G V A T N T F F K P P C V -
 TGTCGGTCTACAGATGTGGGGTTGCTGCAATACTGAGGGCTGCAGTCATGAAACACCA
 481 +-----+
 ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCGACGTCACGTTACTTGTGGGT
 S V Y R C G C N S E G L Q C M N T S -
 GCACGGAGCTACCTCAGCAAAGACGTTATTGAAATTACAGTGCCTCTCTCAAGGGCCA
 541 +-----+
 CGTGGCTCGATGGAGTCTGGCAATAAACTTAAATGTCACGGAGAGAGTTCCGGGGGT
 T S Y L S K T L F E I T V P L S Q G P K -
 AACCACTAACATCAGTTGCCAATCACACTTCTGCCGATGCTAAACTGGATG
 601 +-----+
 TTGGTCATGTGTTAGTCAAACGGTTAGTGTGAAGGACGGCTACGTTGACCTAC
 P V T I S F A N H T S C R C M S K L D V -
 MATCH WITH FIG. 1C

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MATCH WITH FIG. 1C



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MATCH WITH FIG. 1B

661	TTTACAGACAAGTTCATTCATTAGACGTTCCATTCCCTGCCAGGAAACACTTACCAACAGTC	720
	AATGTCCTGTTCAAGGTAAATCTGCAGGGACCCCTGGTGTGATGGTGTACACG	
	Y R Q V H S I I R R S L P A T L P Q C Q -	
721	AGGCAGCGAACAGACCTGGCCCCACCAATTACATGGAAATAATCACATCTGCAGATGCC	780
	TCCGTCGCTTGTCTGGACGGGGGGTTAATGTACACCTTATTAGTGTAGACGTTACCGG	
	A A N K T C P T N Y M W N N H I C R C L -	
781	TGGCTCAGGAAGAGATTATGTTTCTCGGATGGAGATGACTCAAACAGATGGATTCC	840
	ACCGAGTCCTCTAAATAACAAAGGAGCCTACCGACCTACTGAGTTGTCTACCTAAGG	
	A Q E D F M F S S D A G D D S T D G F H -	
841	ATGACATCTGTGGACCAACAGGAGGCTGGATGAGAGACCTGTCAGTGTCAGTGAGAG	900
	TACTGTAGACACCTGGTTCTCGACCTACTTCTGGACAGTCACACAGACGTCTC	
	D I C G P N K E L D E E T C Q C V C R A -	
901	CGGGGCTTGGCCTGCCAGCTGGACCCACAAAGAAACTAGACAGAAACTCATGCCAGT	960
	GCCCCGAAGCCGGACGGTCTGACACCTGGGTGTTCTGATCTGTTGAGTACGGTCA	
	G L R P A S C G P H K E L D R N S C Q C -	
961	GTGTCGTAAAACAAACTCTTCCCCAGCCAATGTGGGGCAACCGAGAATTGATGAAA	1020
	CACAGACATTTTGTGAGAAGGGCTGGTTACACCCCCCTGGTCTCTTAACCTACTTT	



MATCH WITH FIG. 1C

V C K N K L F P S Q C G A N R E F D E N -

ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021 ---+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
TGTGTACCGGTACACATACATTCTGGACGGGGTCTTTAGTTGGGATTAGGACCTT
T C Q C V C K R T C P R N Q P L N P G K -

AATGTGCCCTGTGAATGTACAGAACAGAACATGCTTGTAAAGGAAAGAAGTTCC
1081 ---+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
TTACACGGACACTTACATGTCTTCAGGTGTCTTTACGAAACAATTCTTCCTTCAAGG
C A C E C T E S P Q K C L L K G K F H -

ACCACCAACATGCCAGCTGTTACAGACGGCCATGTACGAAACGCCAGAACGGCTGTGAGC
1141 ---+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
TGGTGGTTGTACGGTGCACAATGTCTGCCGGTACATGCTTGGCCGGTCTTCGAAACACTCG
H Q T C S C Y R R P C T N R Q K A C E P -

CAGGATTTCATATAAGTGAAGAAGTGTGTCGTTGTGTCCCTCATATGGCAAAGACCCAC
1201 ---+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
GTCCTAAAGTATATCACTTCTCACACAGCAACAGGAAGTATAACCGTTCTGGTG
G F S Y S E E V C R C V P S Y W Q R P Q -

AAATGAGCTAAGATTGTACTGTTCCAGTTCATCGATTCTTCTATTATGGAAAAGTGTGT

MATCH WITH FIG. 1E

FIG. 1D



MATCH WITH FIG: 1D

1261 TTTACTCGATTCTAACATGACAAAGGTCAAGTAGCTAAAAGATAATAACCTTTGACACA
M S *

CAAAAGGCCTCTTGTAAAGACTGGTTCTGCCAATGACCAAACAGCCAAAGATTTCCTC	-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+	11441	-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+	1500
GTTTTCGGAGAACATTCTGACCAAAAGACCGTTACTGGTTTGTCTGTTAAAAGGAG				

TTGTGATTCTTAAAAGAATGACTATAATTATTCCACTAAAAATAATTGTTCTGC	-----+-----+-----+-----+-----+-----+-----+-----+-----+	1560
AACACTAAAGAAATTCTTACTGATAATAAAAGGTGATTTTATAACAAAAGCC	-----+-----+-----+-----+-----+-----+-----+-----+-----+	1501

621 GCAAAATATGTTAAAATAAATGAAATTTGTATTATAAAAAAA
CGTTTATACAAATTATTTACTTTAACATAATAATTCTT

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1 CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGCAGTTACGGTCTGTGTCAGTGT
- - - - + - - - + - - - + - - - + - - - + - - - +
71 AGATGAACTCATGACTGTACTCTACCCAGAAATATTGAAAATGTACAAGTGTCAAGCTAAG
- - - - + - - - + - - - + - - - + - - - + - - - +
M T V L Y P E Y W K M Y K C Q L R
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGCACAGAAAGAGAC
- - - - + - - - + - - - + - - - + - - - + - - - +
K G G W Q H N R E Q A N L N S R T E E T
181 TATAAAATTGCTGCAGGCACATTAAATACAGAGATCTGAAAAGTATTGATAATGAGTG
- - - - + - - - + - - - + - - - + - - - + - - - +
I K F A A H Y N T E I L K S I D N E W
241 GAGAAAGACTCAATGCATGCCACGGGAGGGTGTATAGATGTGGGAAGGGAGTTGGAGT
- - - - + - - - + - - - + - - - + - - - + - - - +
R K T Q C M P R E V C I D V G K E F G V
301 CGCGACAAACACCTTCTTAAACCTCCATGTGTGTCGTCAGATGTGGGGTTGCTG
- - - - + - - - + - - - + - - - + - - - + - - - +
A T N T F F K P P C V S V Y R C G G C C C

FIG. 2A

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361 CAATAGTGGGGCTGCAGTCATGAAACACCCAGCACGGCTACCTCAGCAAGAACGTTATT
-+-----+-----+-----+-----+-----+-----+-----+-----+
N S E G L Q C M N T S T S Y L S K T L F

421 TGAAATTACAGTGCCCTCTCTCAAGGGCCCAAACCGTAACAATCAGTTTGCCTAACATCA
-+-----+-----+-----+-----+-----+-----+-----+-----+
E I T V P L S Q G P K P V T I S F A N H

481 CACTTCCTGCCGATGCATGTCATAACTGGATGTTCAGACAAGTCATTCCATTATTAG
-+-----+-----+-----+-----+-----+-----+-----+-----+
T S C R C M S K L D V Y R Q V H S I I R

541 ACGTTCCCTGCCAACACTACCACAGTCAGGGCAGCCGAACAAAGACCTGCCACCAA
-+-----+-----+-----+-----+-----+-----+-----+-----+
R S L P A T L P Q C Q A A N K T C P T N

601 TTACATGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTITATGTTTCCCTC
-+-----+-----+-----+-----+-----+-----+-----+-----+
Y M W N N H I C R C L A Q E D F M F S S

661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAGGAGCT
-+-----+-----+-----+-----+-----+-----+-----+-----+

FIG. 2B



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721 GGATGAAAGACCTGTCAGTGTCTGCAGAGGGCTTCGGCCTGCCAGCTGTGGACC
- - - + + - - + - - + - - + - - + - - + - - +
D E E T C Q C V C R A G L R P A S C G P

781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTCTGTAAAACAACTCTCCCCAG
- - - + + - - + - - + - - + - - + - - +
H K E L D R N S C Q C V C K N K L F P S

841 CCAATGTTGGGCCAACCGAGAATTGATGAAAACACATGCCAGTGTATGTAAAGAAC
- - - + + - - + - - + - - + - - + - - +
Q C G A N R E F D E N T C Q C V C K R T

901 CTGCCCCAGAAATCAACCCCTAAATCCTGGAAATGTGCCTGTGAATGTACAGAAAGTCC
- - - + + - - + - - + - - + - - + - - +
C P R N Q P L N P G K C A C E C T E S P

961 ACAGAAATGCTTGTAAAGGAAGTTCACACCAAAACATGCCAGCTGTACAGACG
- - - + + - - + - - + - - + - - +
Q K C L L K G K F H H Q T C S C Y R R

1021 GGCATGTACGAAACGGCCAGAAGGCTTGTGAGCCAGGATTTCATATAGTGAAGAAGTGTG
- - - + + - - + - - + - - + - - +
P C T N R Q K A C E P G F S Y S E E V C

FIG. 2C



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| | |
|------|--|
| 1081 | TCGTTGTGCCCTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTA
- + - - + - + - - + - - + - - + - - + - - + - - + - - + |
| | R C V P S Y W Q R P Q M S |
| 1141 | GTTCATGGATTCTTATTATGGAAAACTGTGTTGCCACAGTAGAACAGA
- + - - + - + - - + - - + - - + - - + - - + - - + - - + |
| | |
| 1201 | GAGACCCTTGTGGTCCATGCTAACAAAGACAAAGTCTGTCTGAACCATGTGGA
- + - - + - + - - + - - + - - + - - + - - + - - + - - + |
| | |
| 1261 | TAACTTACAGAAATGGACTGGAGCTCATCTGCCAAAAGGCCCTCTGTAAAGACTGGTTT
- - - - + - - + - - + - - + - - + - - + - - + - - + - - + |
| | |
| 1321 | CTGCCAATGACCAAACAGCCAAGATTTCCTGTGATTCTAAANGAATGACTATA
- - - - + - - + - - + - - + - - + - - + - - + - - + - - + |
| | |
| 1381 | TAATTATTCCACTAAAATATTGTTCTGCATTCAATTATAGCAACAAATTGGT
- - - - + - - + - - + - - + - - + - - + - - + - - + - - + |
| | |
| 1441 | AAAACCTCACTGTGATCAATAATTCTTATCATGCAAAATAATGTTAAATGAAAA
- - - - + - - + - - + - - + - - + - - + - - + - - + - - + |
| | |
| 1501 | TTGTATTATAAAAAAA
- - - - + - - + - - + - - + - - + - - + - - + - - + - - + |

FIG. 2D



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1 Pdgfa MRTLACLLL LGGYLAHVL AEEAEIPREV IERLARSQIH SIRDQLORLLE
Pdgfb MNRCWA.LFL SLCCYRLVS AEGDPipeel YEMLSDHSIR SFDDLQRLLH
Vegf MNFLL SWVHWISLALL LYLHHAKWSQA
Vegf2 MTV LYPEYMKMYK CQLRKGWQHN

50

51 Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHIVEKRP LPIRRKRSI EEAVP
Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
Vegf APMAE GGGQ NHHEVVKFMD VYQR
Vegf2 REQANLNRSRT EETIKFAAAH YNTEILKSID NEWRK.....

100

101 Pdgfa AVCKTRTVIY EIPRSQVQOPT SANFLI~~W~~PPC VEWKRC~~T~~GCC NTSSV~~K~~CAPS
Pdgfb AECKTRTEVF EISRRLIDRT NANFLW~~W~~PPC VEWQRCGGCC NNRNVQCRPT
Vegf SYCHPIETLV DIFQEYPDEI .EYIFKPSC VPLMRCGGCC NDEGLEQVPT
Vegf2 TQCMPREVC1 DVGKEFGVAT .NTFFKPPC VSVYRCGGCC NSEGGLQ~~MNT~~

150

151 Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLEOAO AT
Pdgfb QVQLRPVQVR KIEIVRKPKI FKKATVTLED HLACKO ETVAAPVT
Vegf EESNITMQIM RIK.PH .. QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSGRQMSKL DVYRQVHSII

200

FIG. 3A



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250

Pdgfa TSLNPD YREEDTDOVR.
Pdgfb RSPGGSQEQR AKTPQTRVTI RTVVRRRPK GKHKFKKHTH DKTALKETLG
Vegf RGK GKGQKRKRK KSRYKSWSY VGARCCCLMPW SLPGPHP
Vegf2 RRSLPATLPQ CQAANKTCPT NYMMNNHICR CLAQEDFMFS SDAGDDSTDG

251

Pdgfa
Pdgfb A
Vegf CGP
Vegf2 FHDICGPNE LDEETCQCVC RAGLRPASCG PHKEL... DR NSCQCVCCKNK

301

Pdgfa
Pdgfb
Vegf DSRCKARQ LEINERTCRC DKPRR
Vegf2 LFPSQCGANR EFDENTCQC VCKRTCPRNQ PLNP GKACE CTESPKCLL

351

Pdgfa
Pdgfb
Vegf KGGKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPMWS

FIG. 3B



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PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN
EACH PAIR OF GENES IS SHOWN IN THE
FOLLOWING TABLE

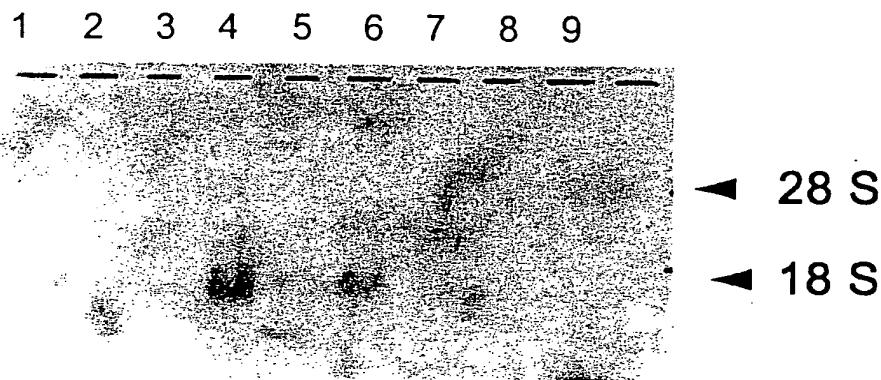
| | PDGF α | PDGF β | VEGF | VEGF2 |
|---------------|---------------|--------------|------|-------|
| PDGF α | | | | |
| PDGF β | 48.0 | | | |
| VEGF | 20.7 | 22.7 | | |
| VEGF2 | 23.5 | 22.4 | 30.0 | |

FIG. 4

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Expression of VEGF2 mRNA in Human Breast Tumor Cells

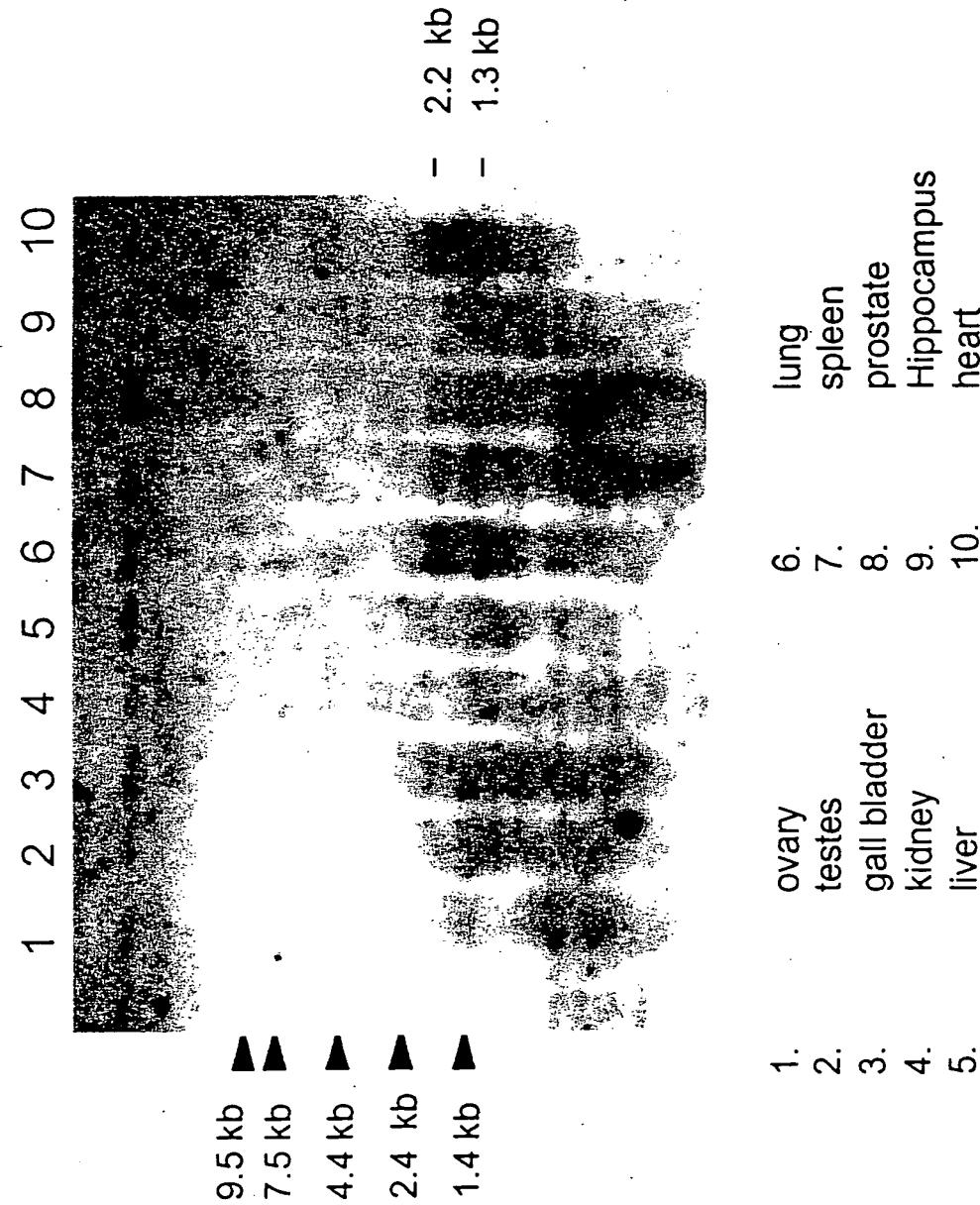


- Lane 1. normal breast tissue
- Lane 2. breast tumor tissue
- Lane 3-9. breast tumor cell lines.

FIG.5



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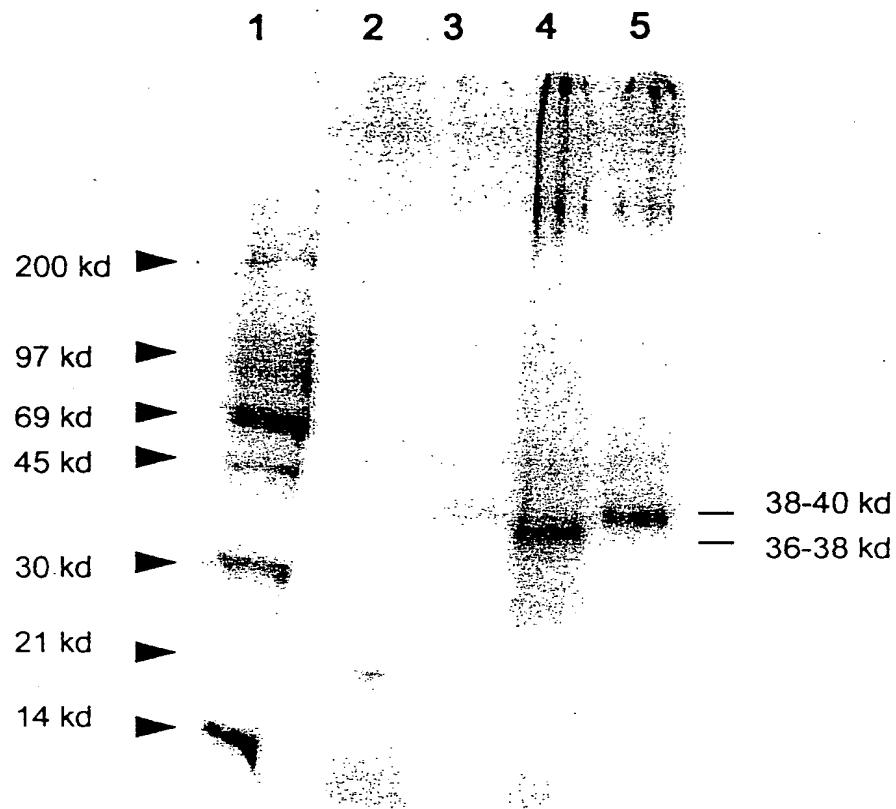


Expression of VEGF2 mRNA in human adult tissues.

FIG. 6



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- Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG. 7

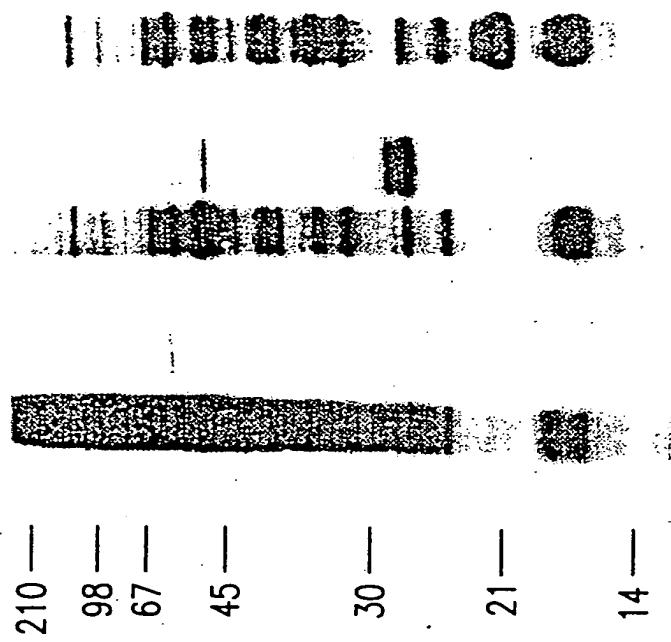
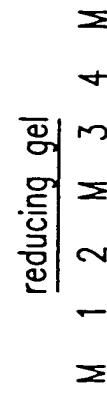


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Lane M: Marker
Lane 1: vector medium
Lane 2: VEGF2 medium

FIG. 8A

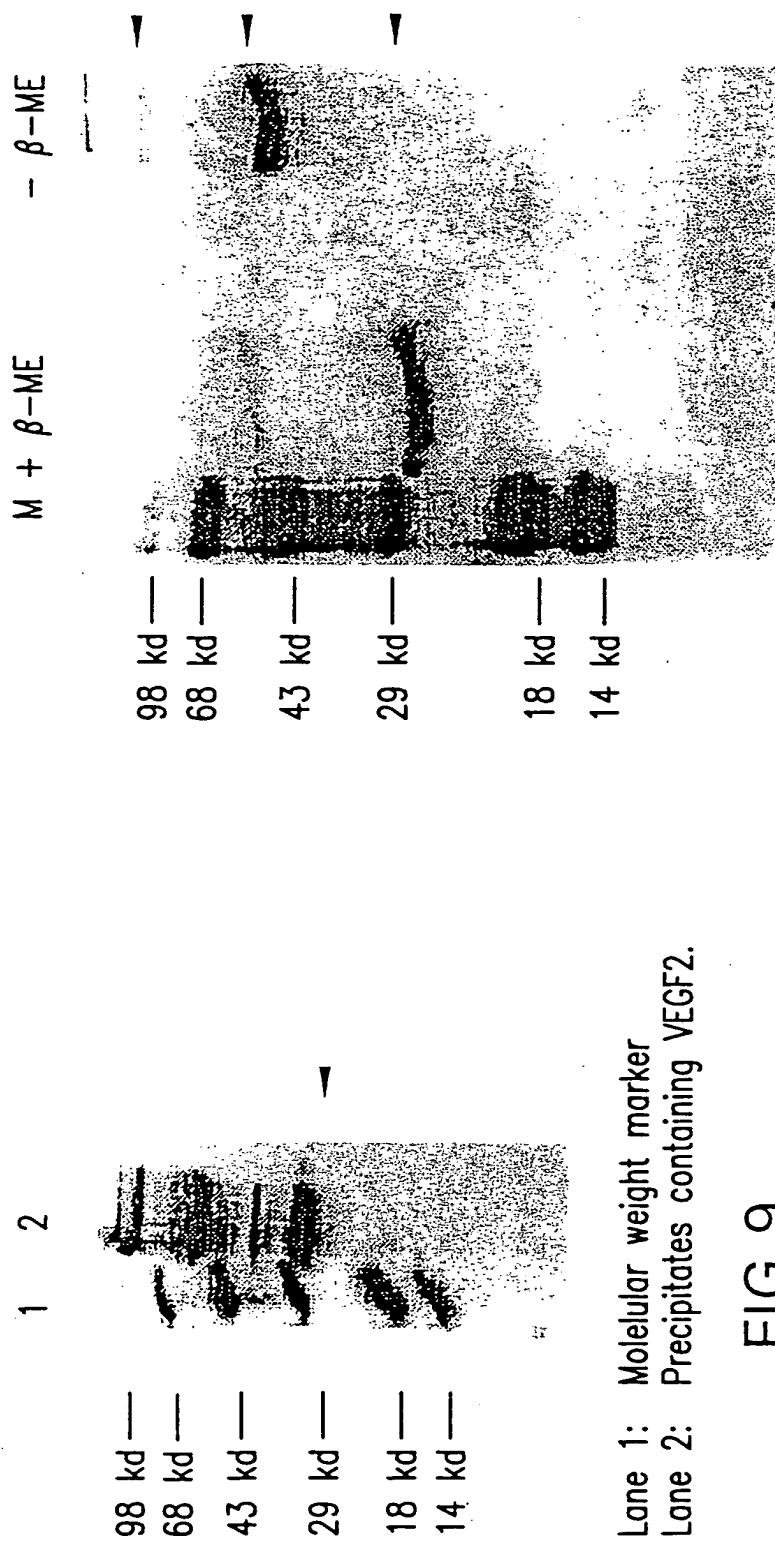


Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

FIG. 8B



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Lane 1: Molecular weight marker
Lane 2: Precipitates containing VEGF2.

FIG. 9

FIG. 10



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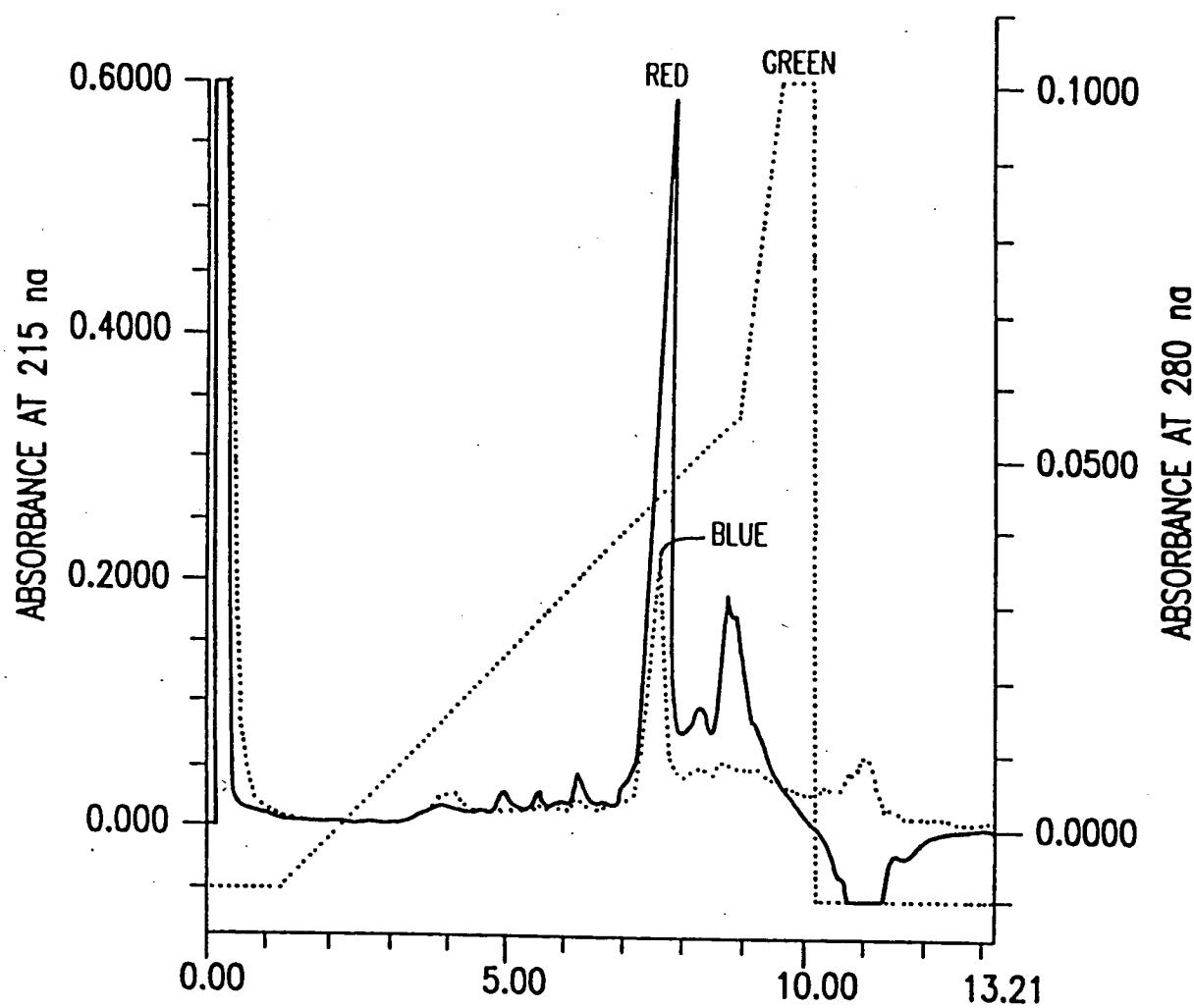


FIG. 11



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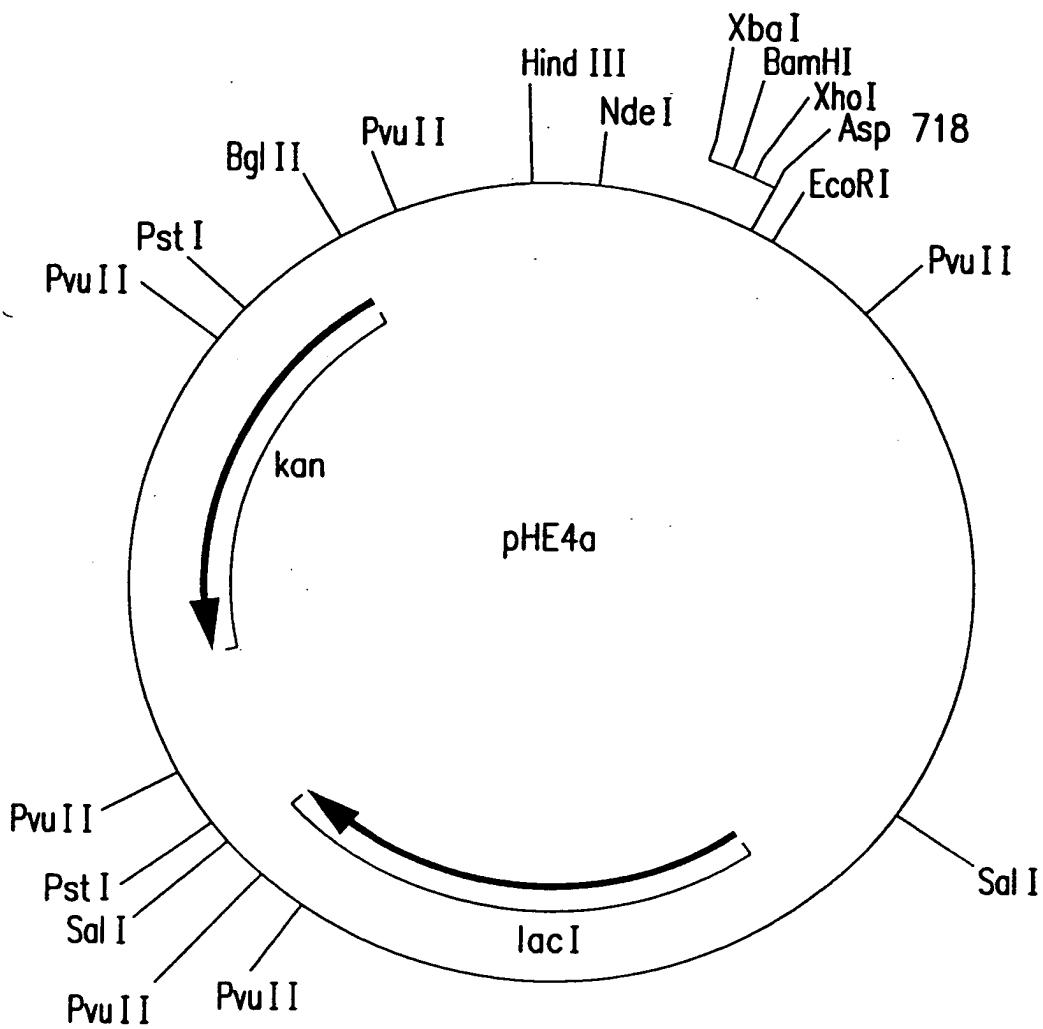


FIG.12



OPERATOR 1

-35

1 A A G C T T A A A A A C T G C A A A A A T A G T [T T G A C T (T G T G A C G G A T A A G A A T A

OPERATOR 2

-10

50 [T A A G A T] G T A C C C A (A T T G T G A G G C G A T A A C A A T) T C A C A C A T T A A

S/D

94 A G A C C A G A A A T T A C A T A T G

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FIG. 13

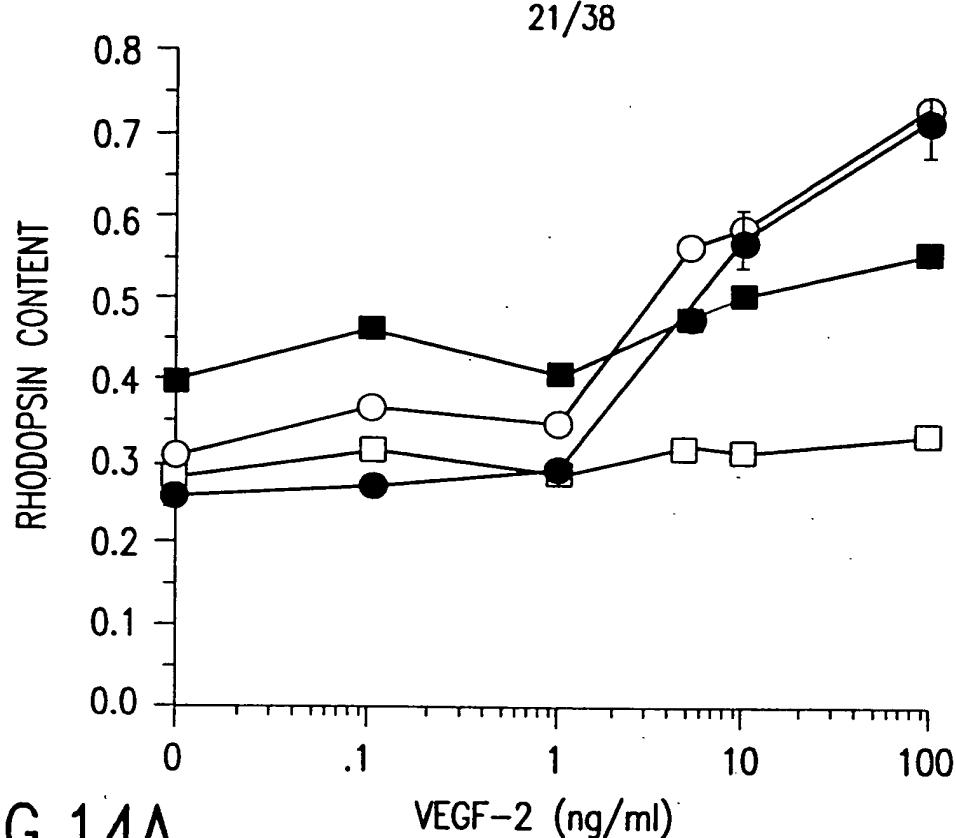


FIG.14A

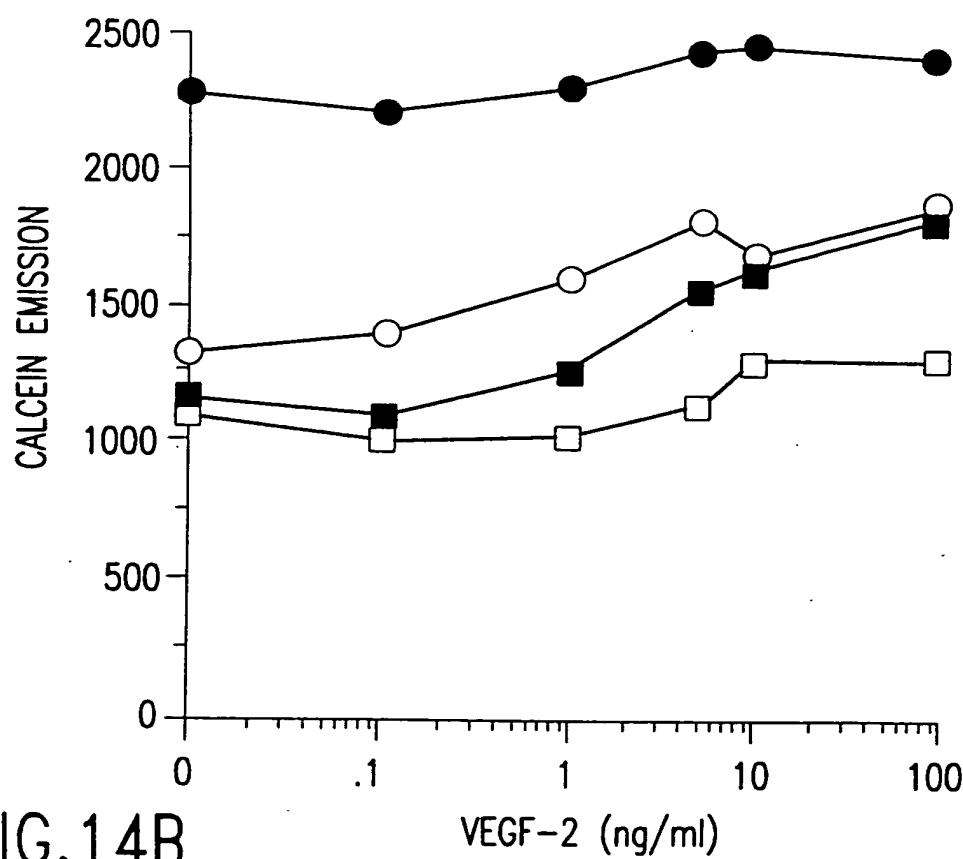


FIG.14B

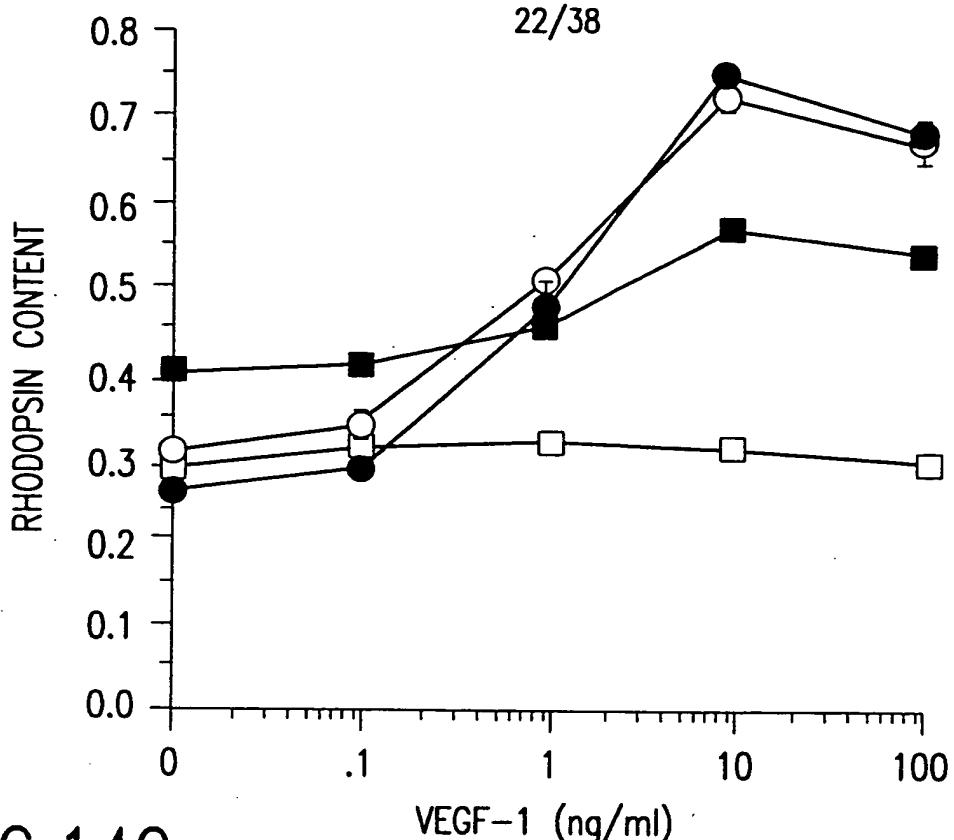


FIG.14C

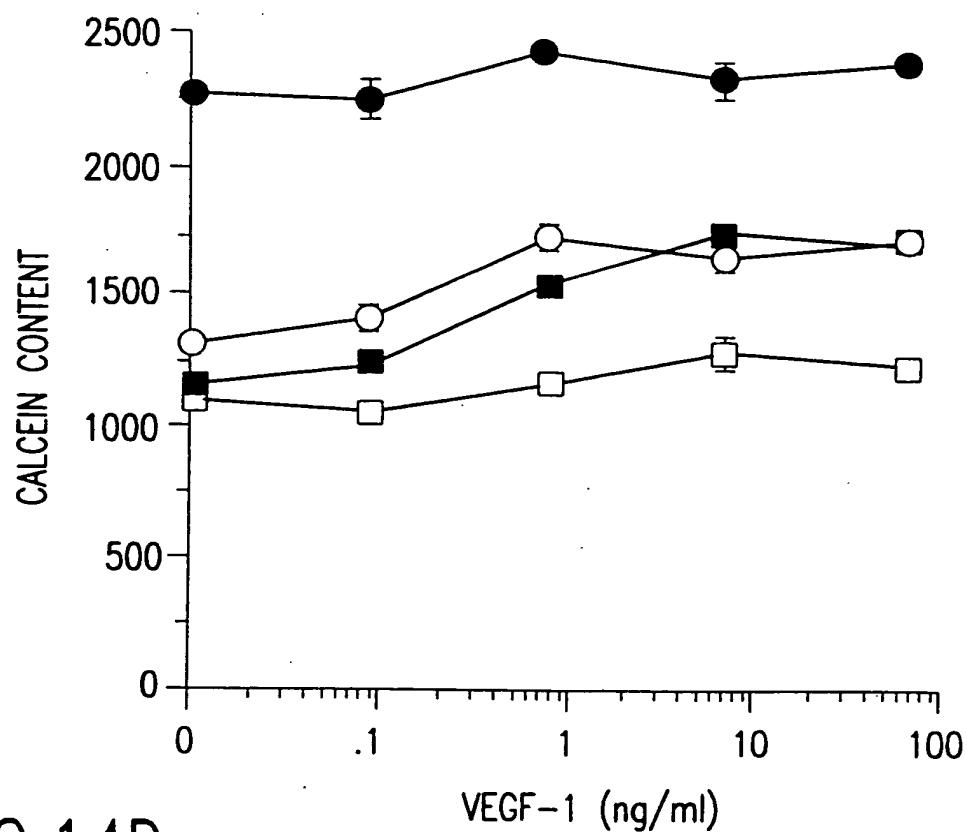


FIG.14D



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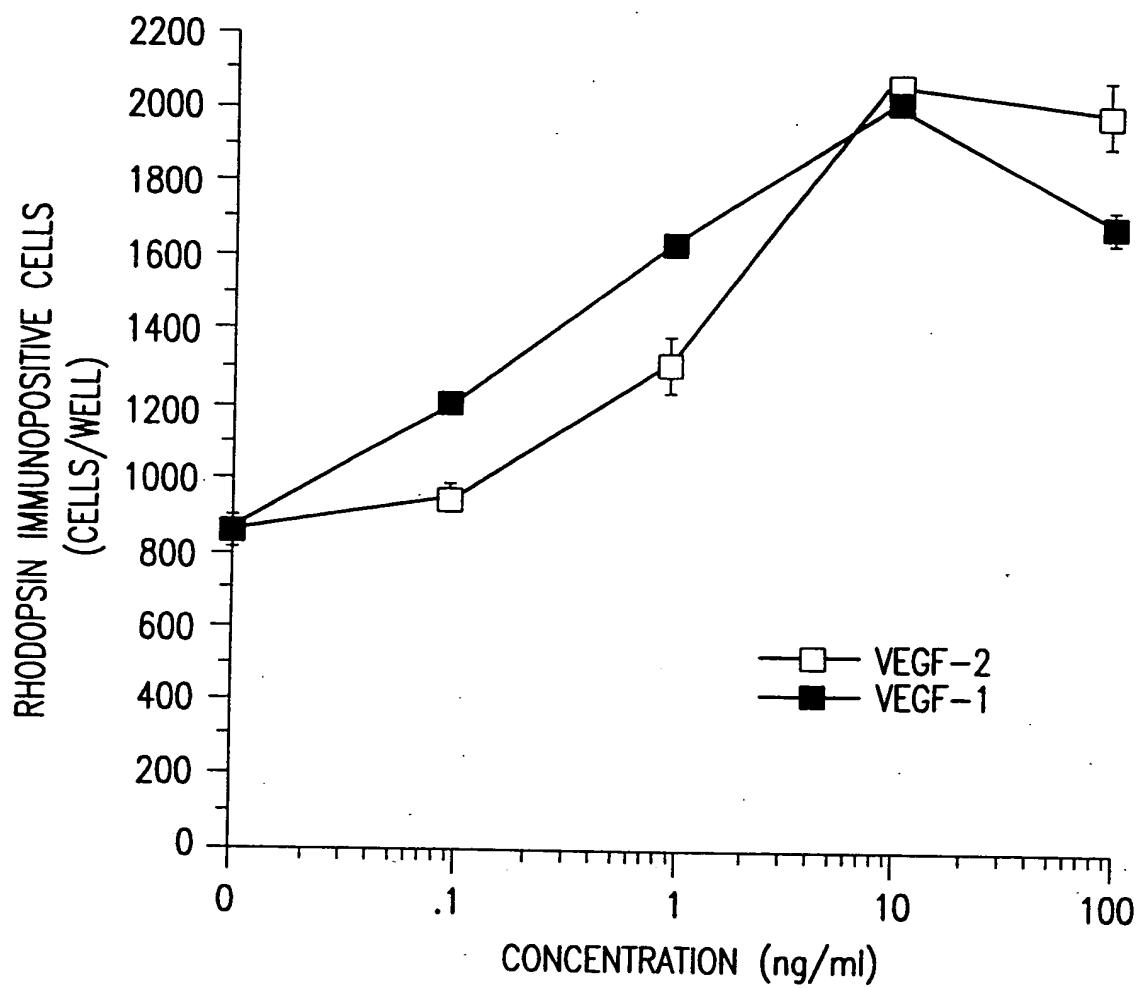


FIG.15

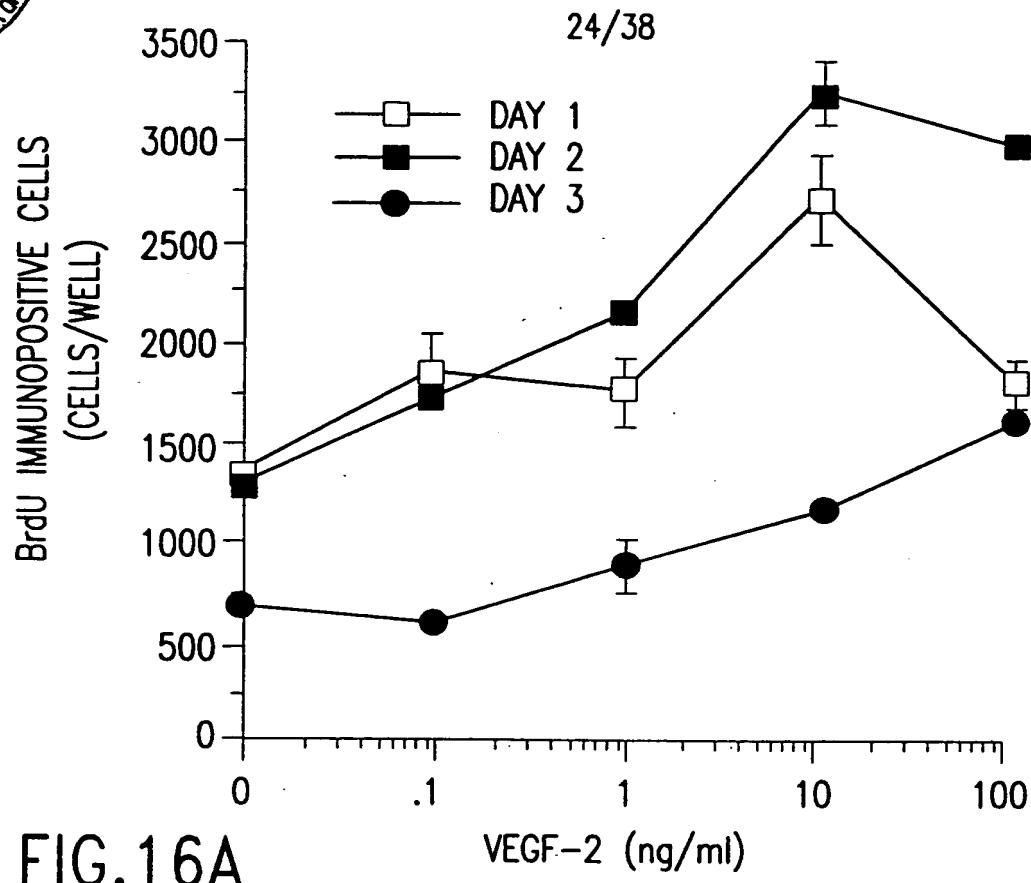


FIG.16A

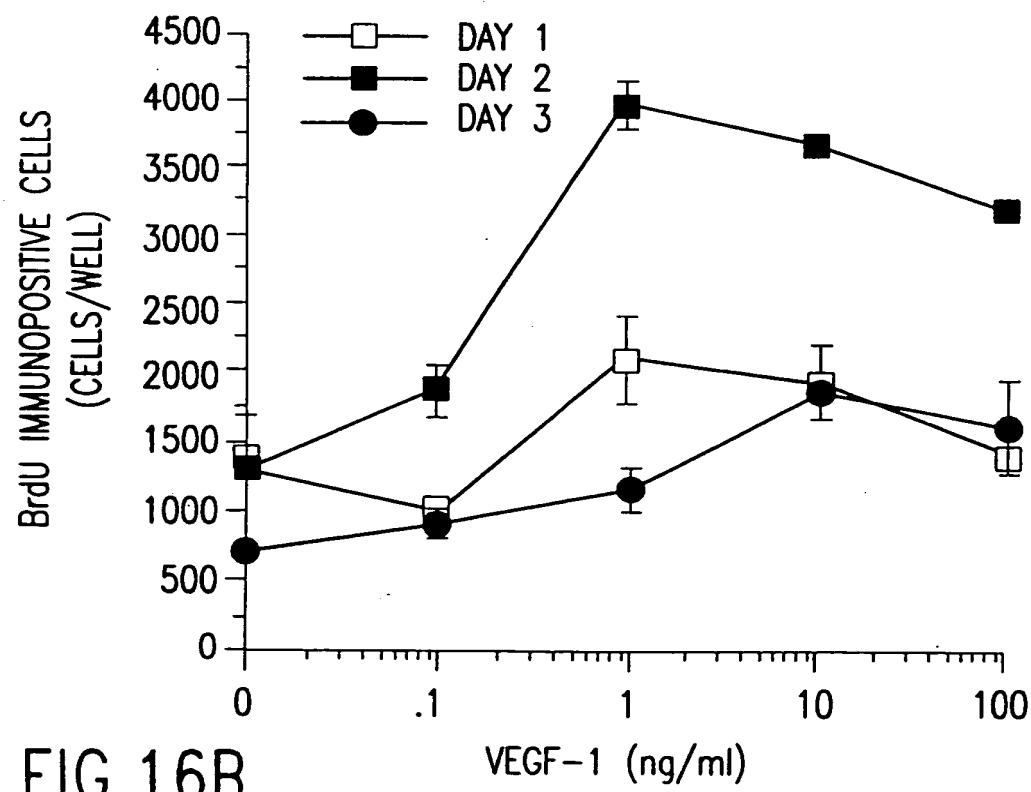


FIG.16B



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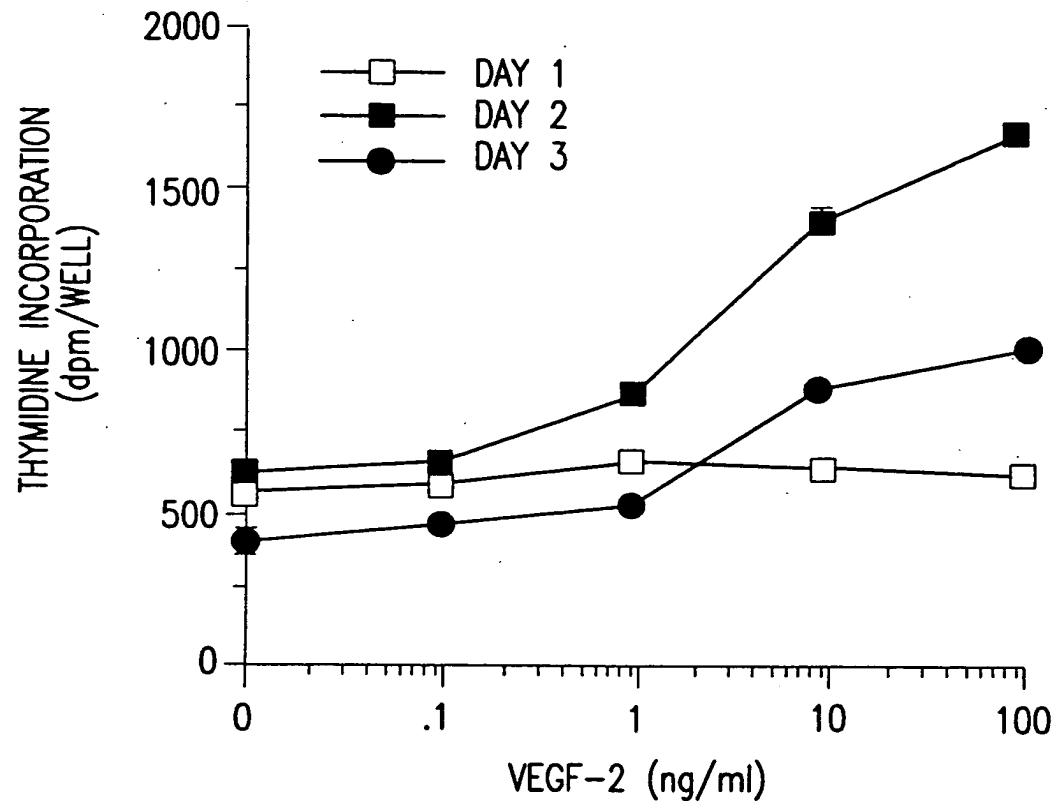


FIG.16C



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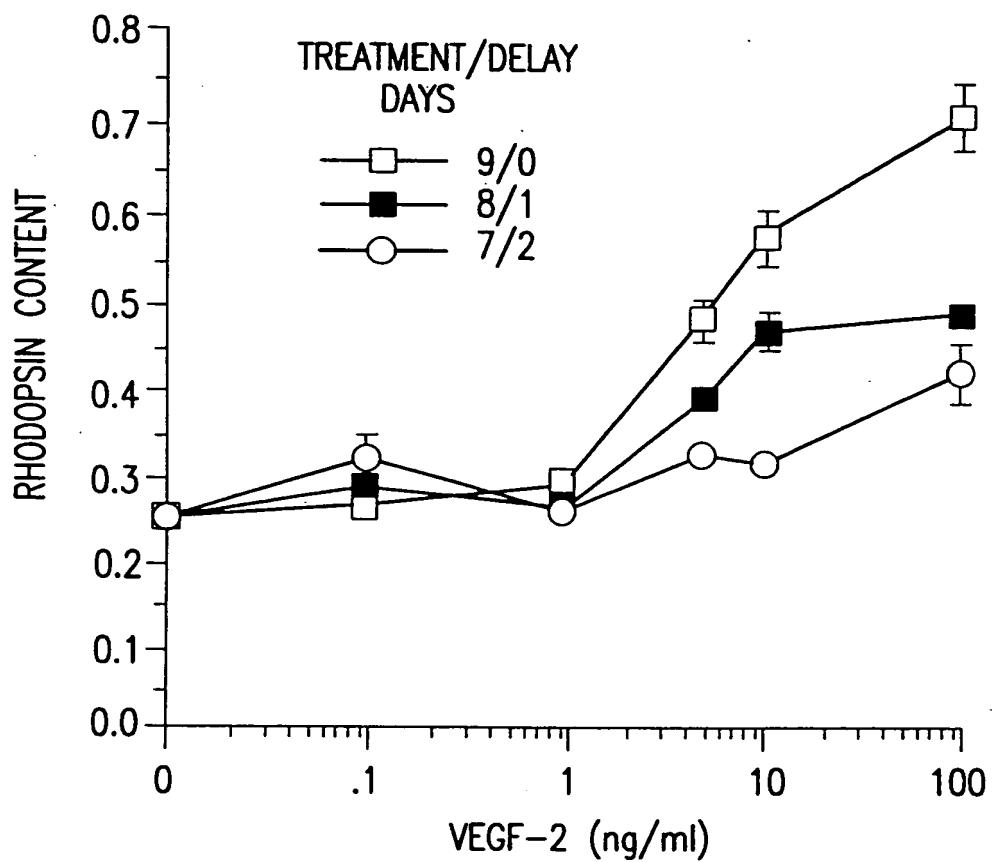


FIG.17A

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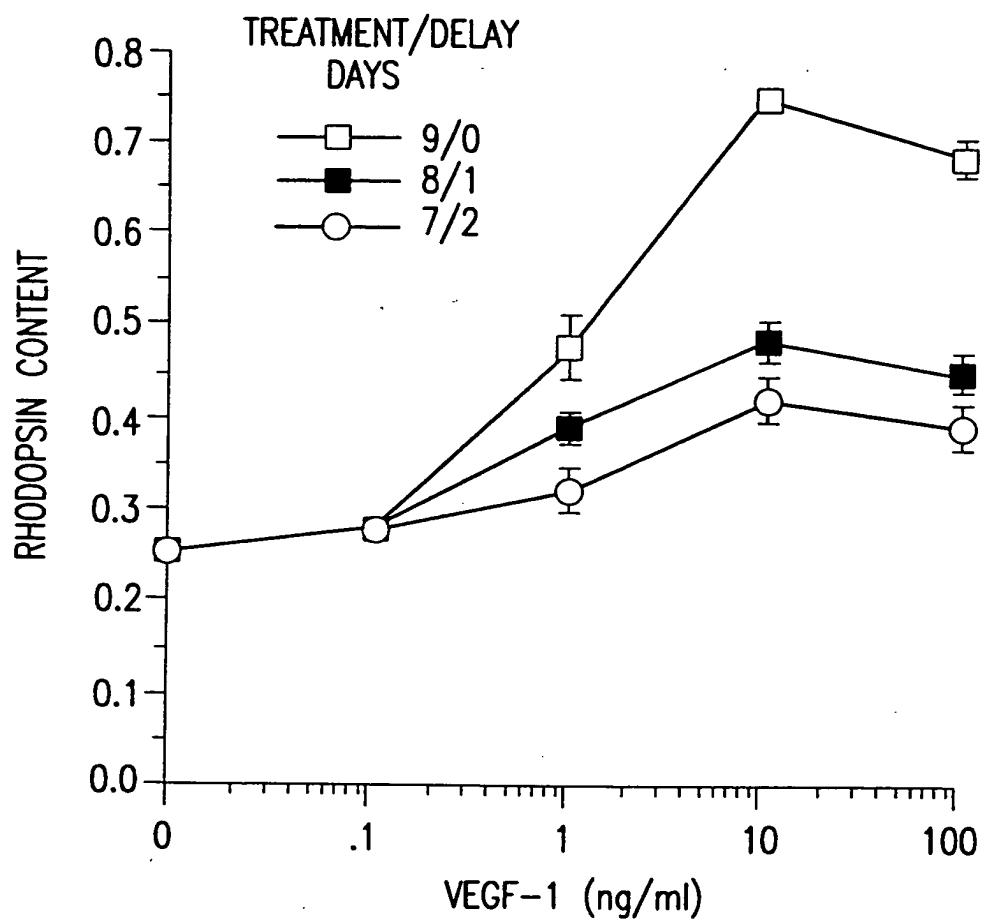


FIG.17B



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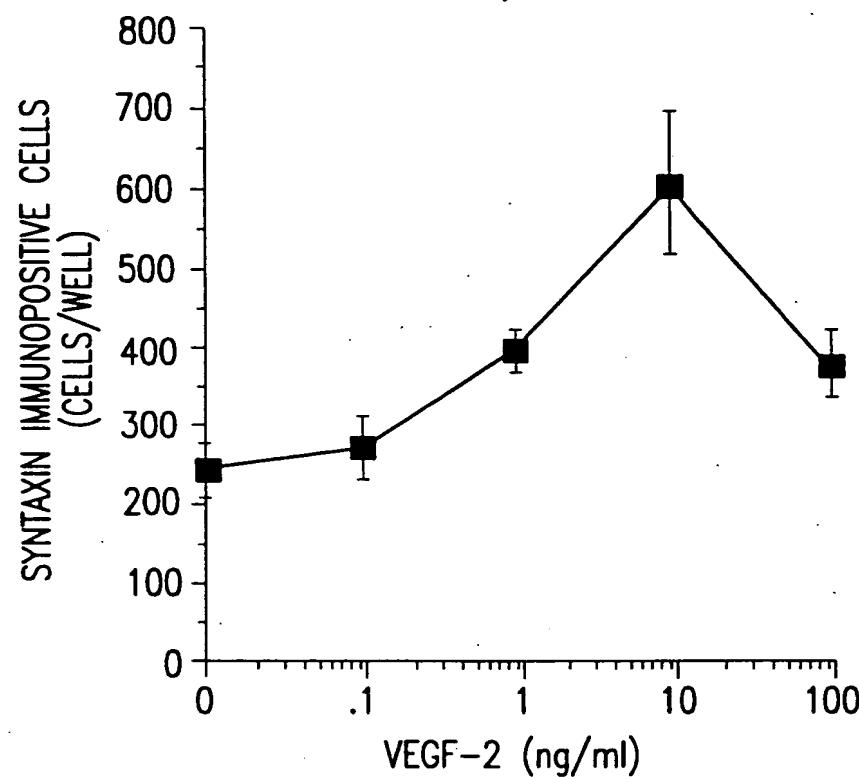


FIG.18A

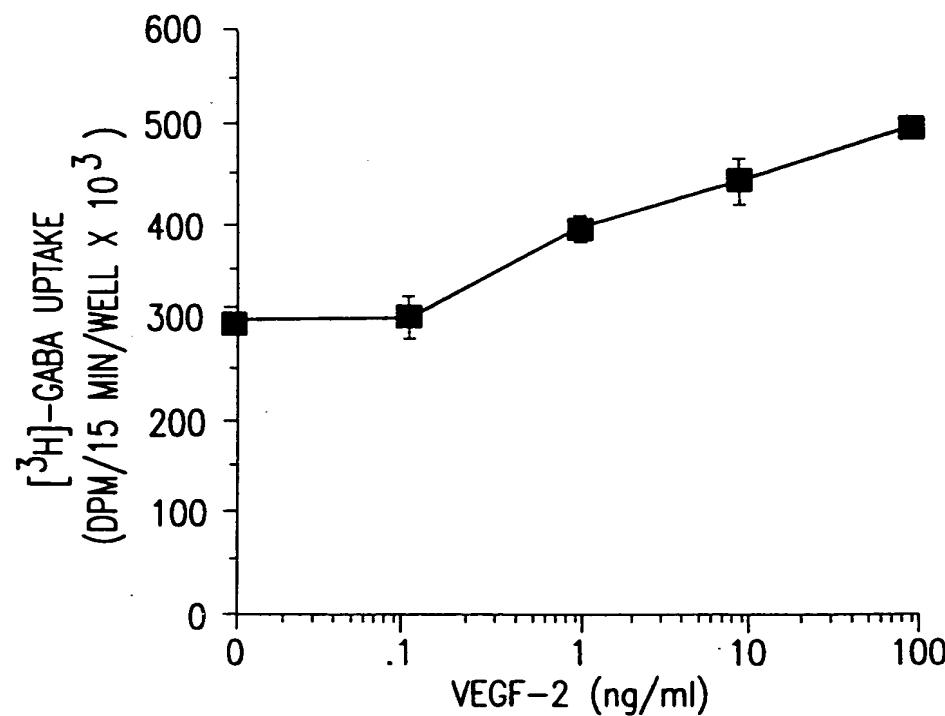


FIG.18B



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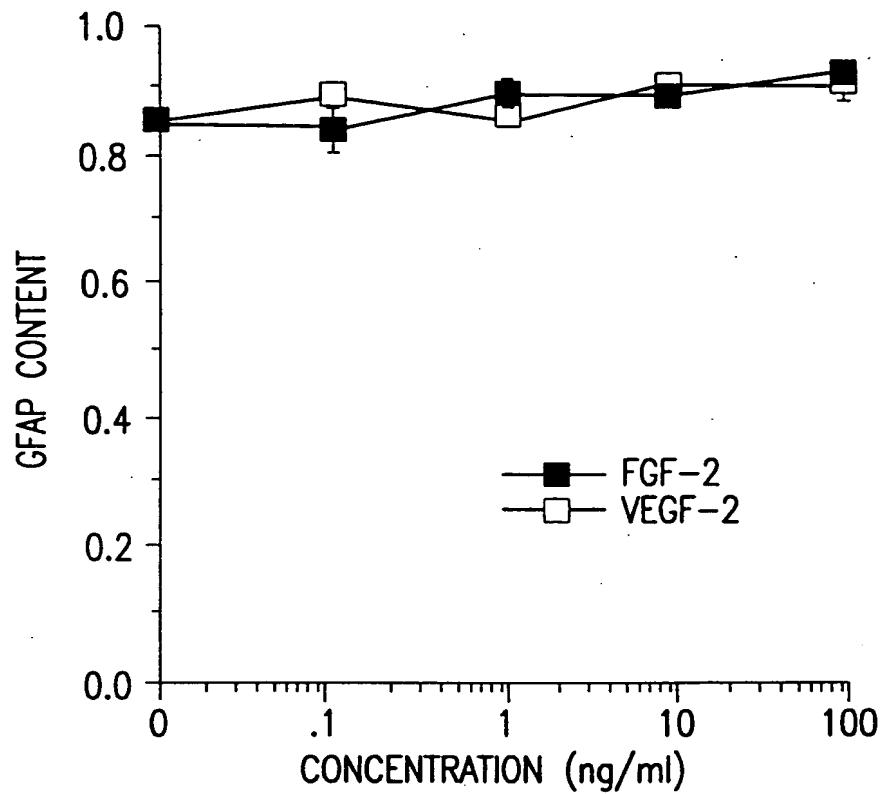


FIG.18C



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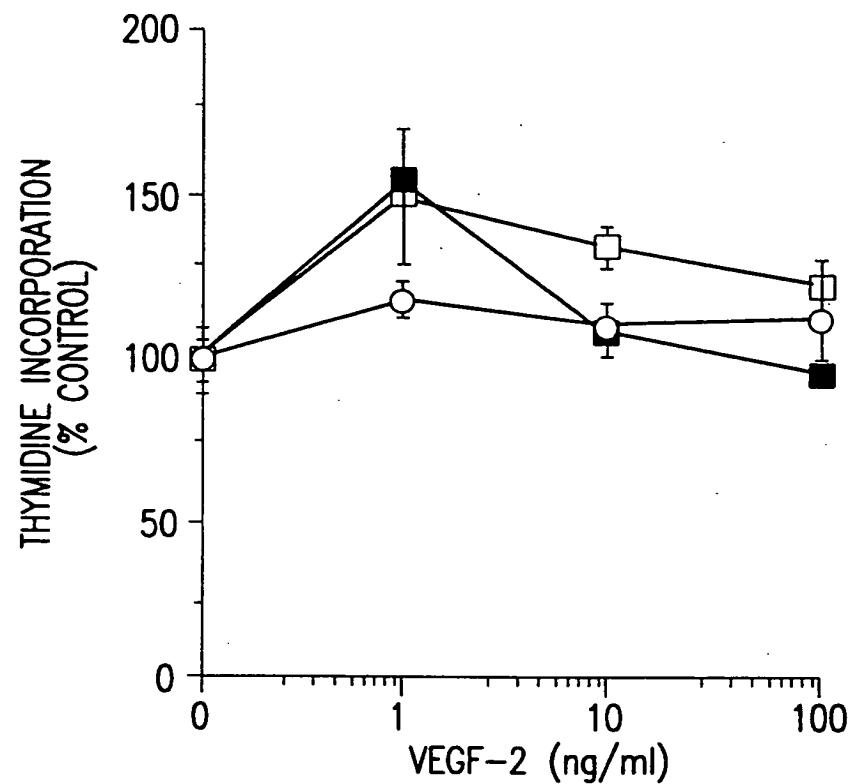


FIG.19A

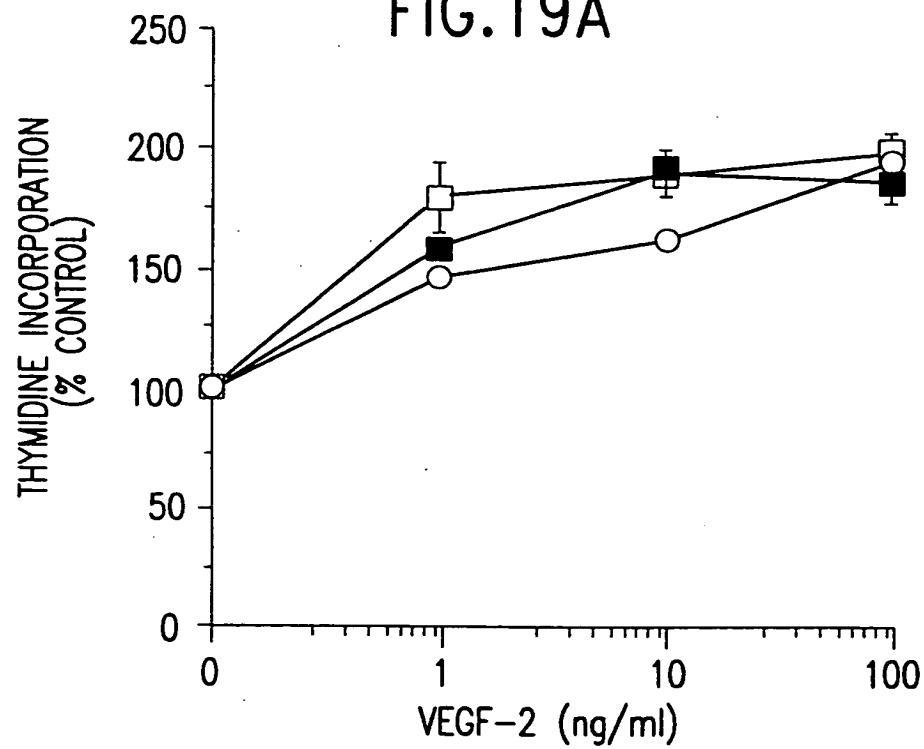


FIG.19B



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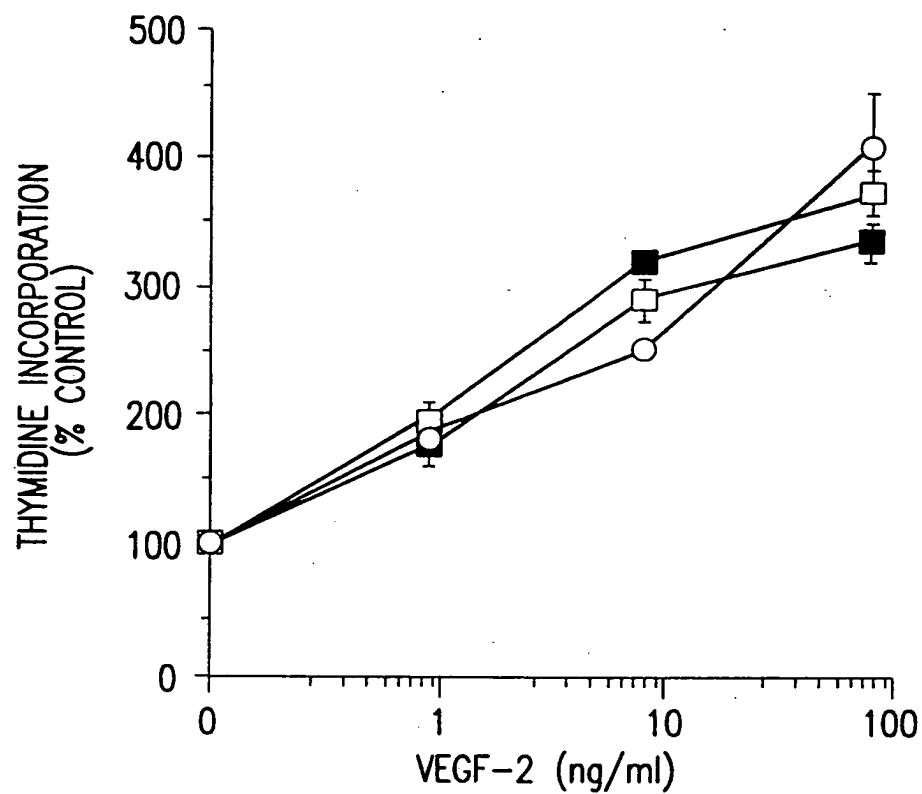


FIG.19C



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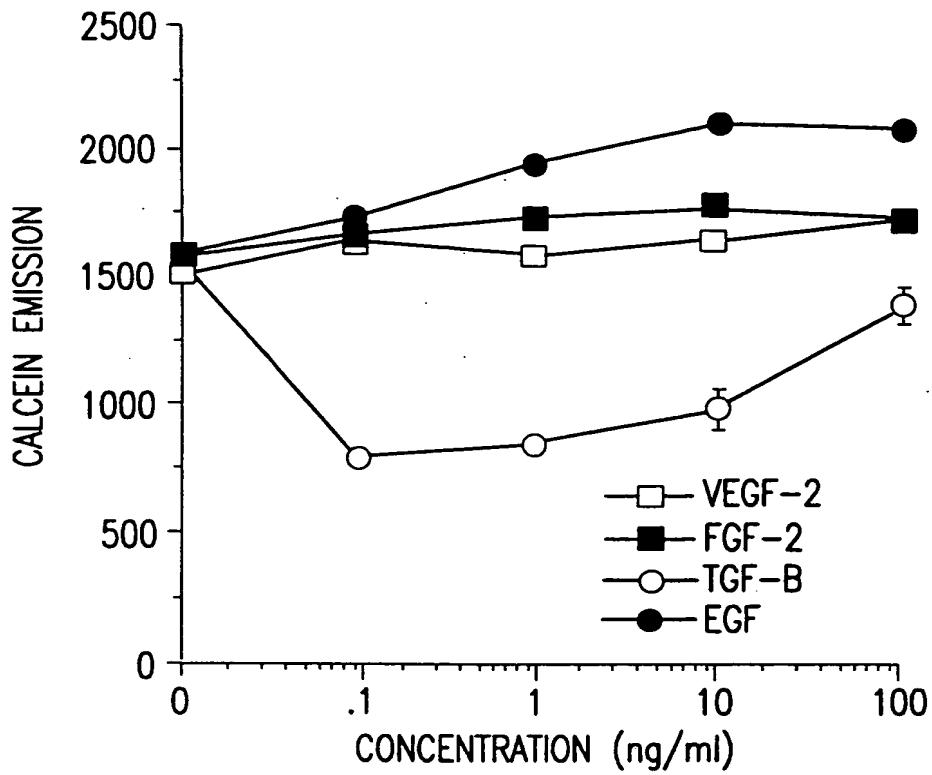


FIG.20A

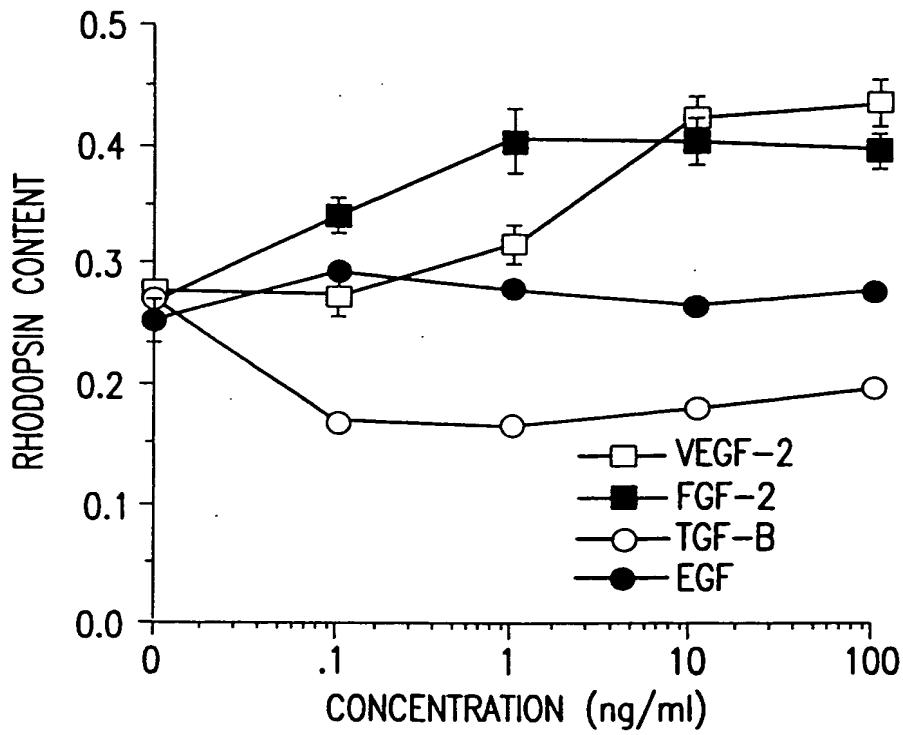


FIG.20B

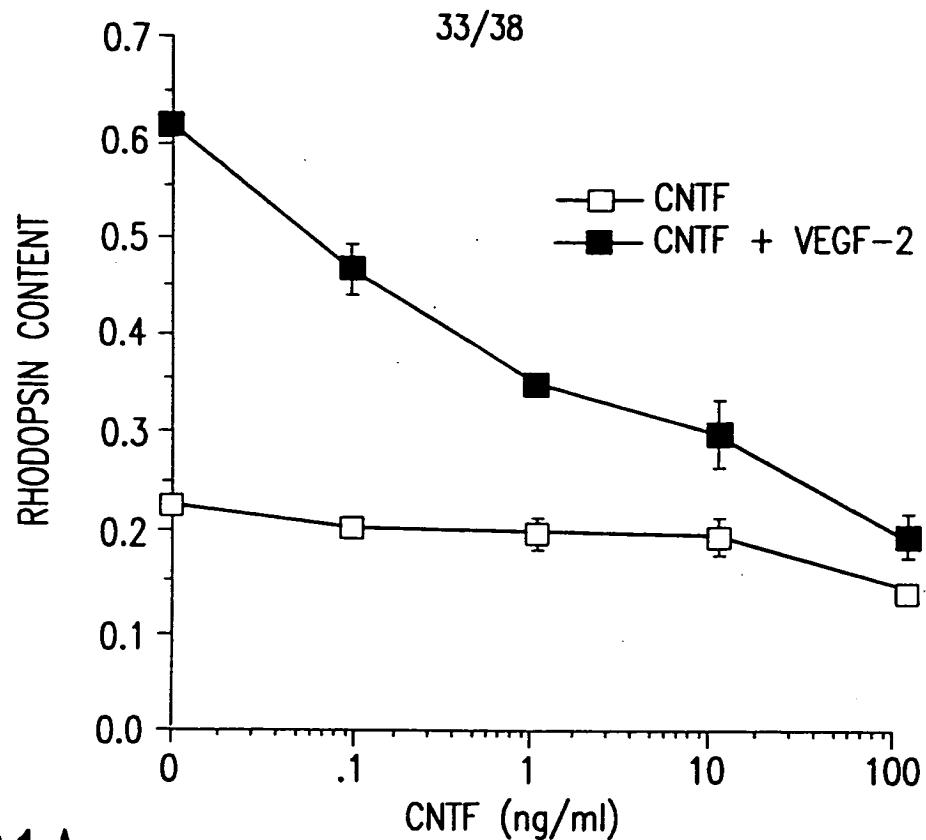


FIG.21A

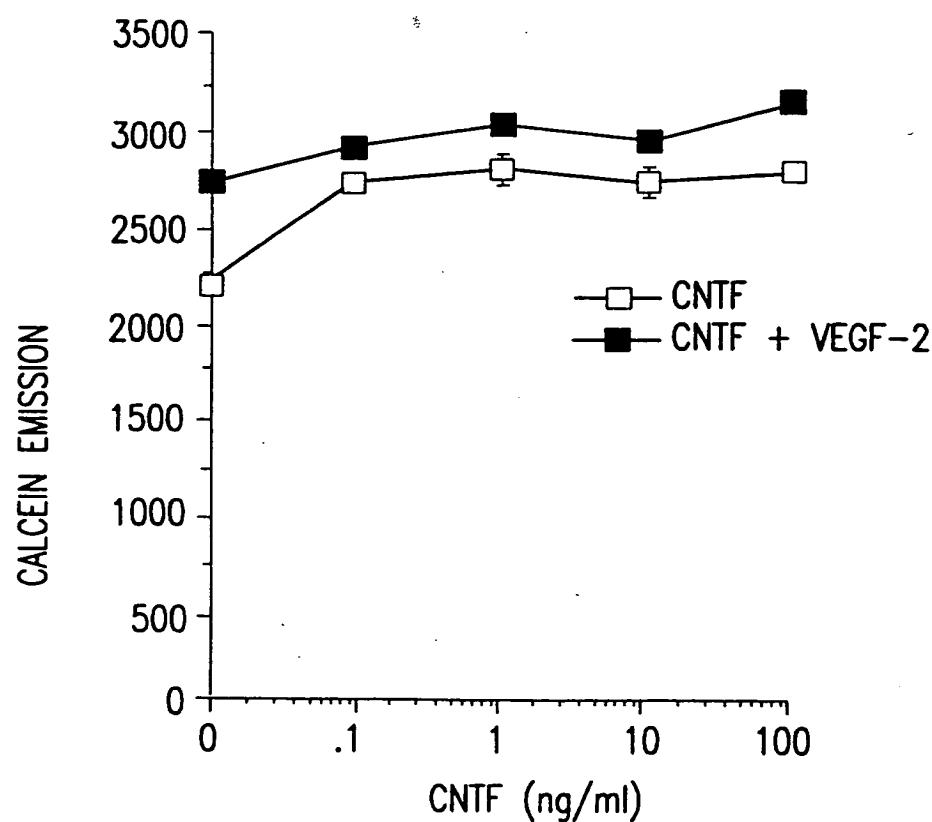


FIG.21B



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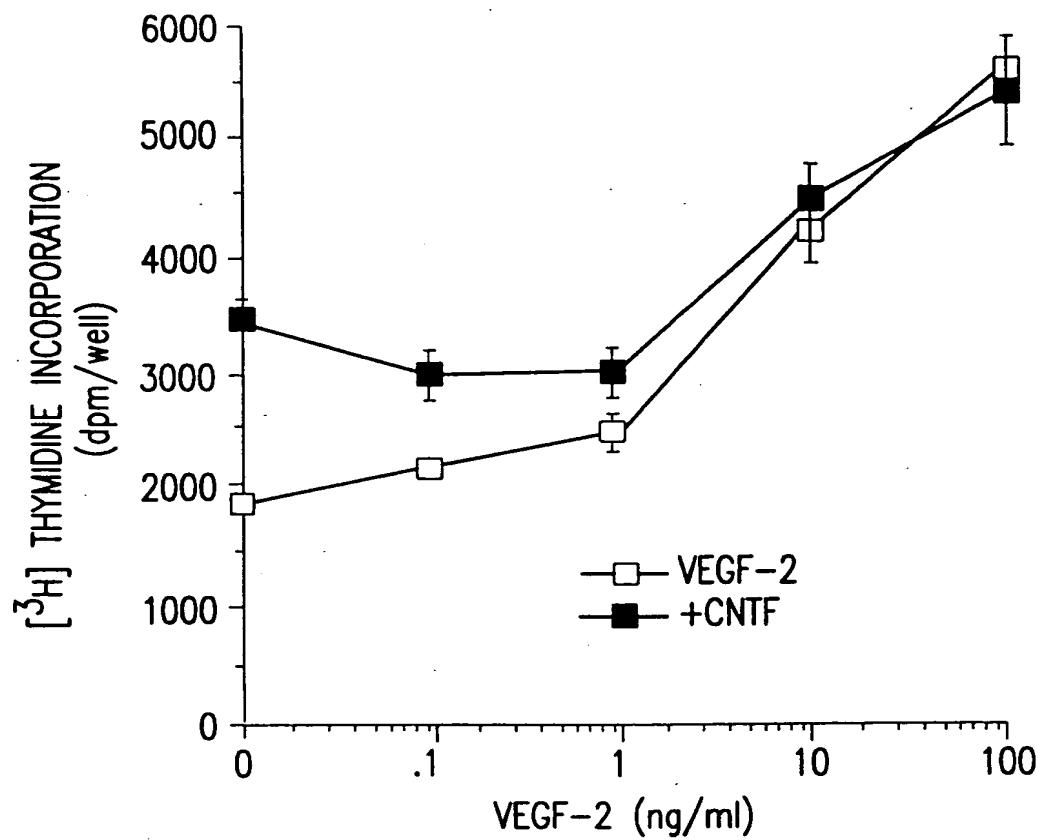


FIG.21C

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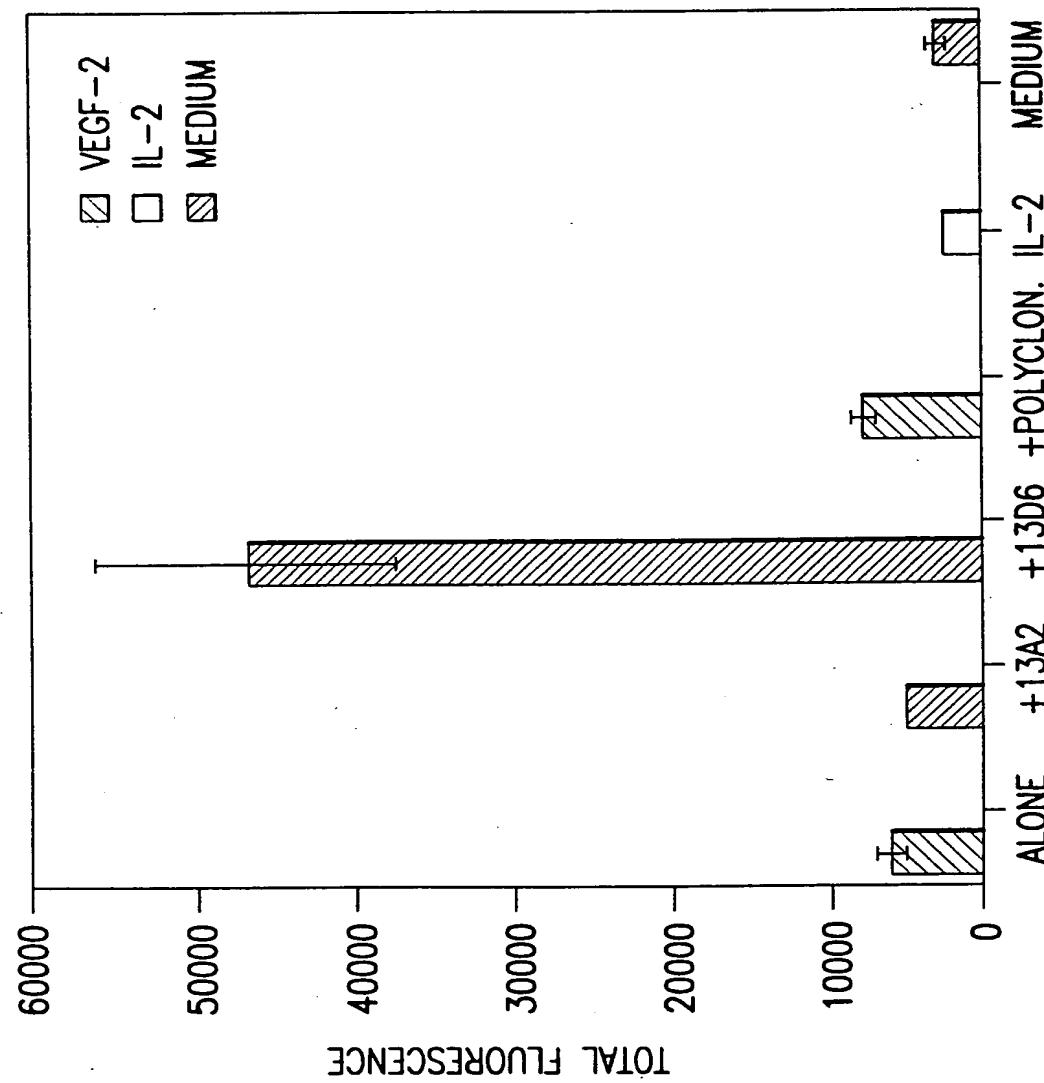


FIG. 22

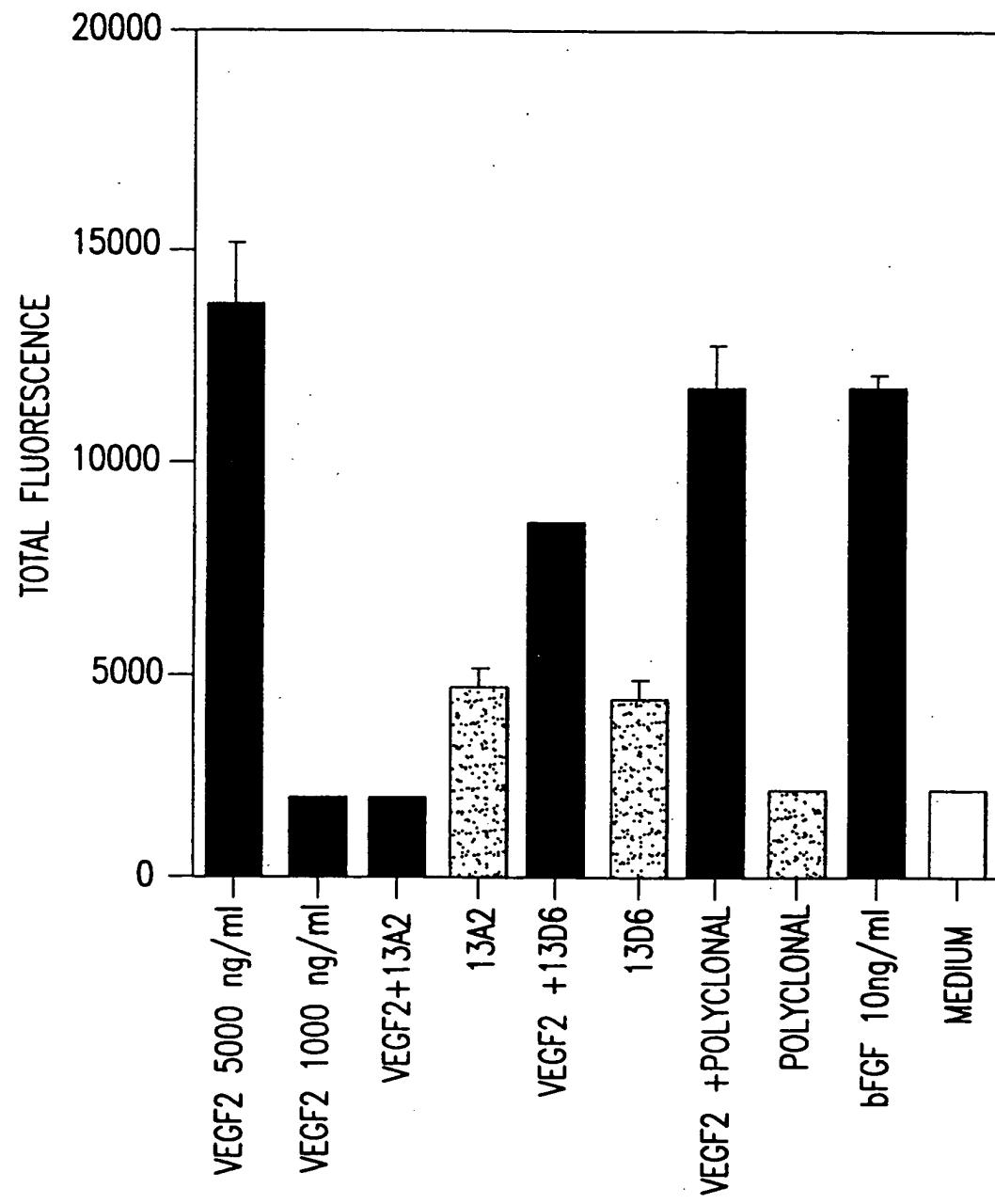


FIG.23



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EPITOPE MAP FOR MURINE ANTI VEGF-2 MAB

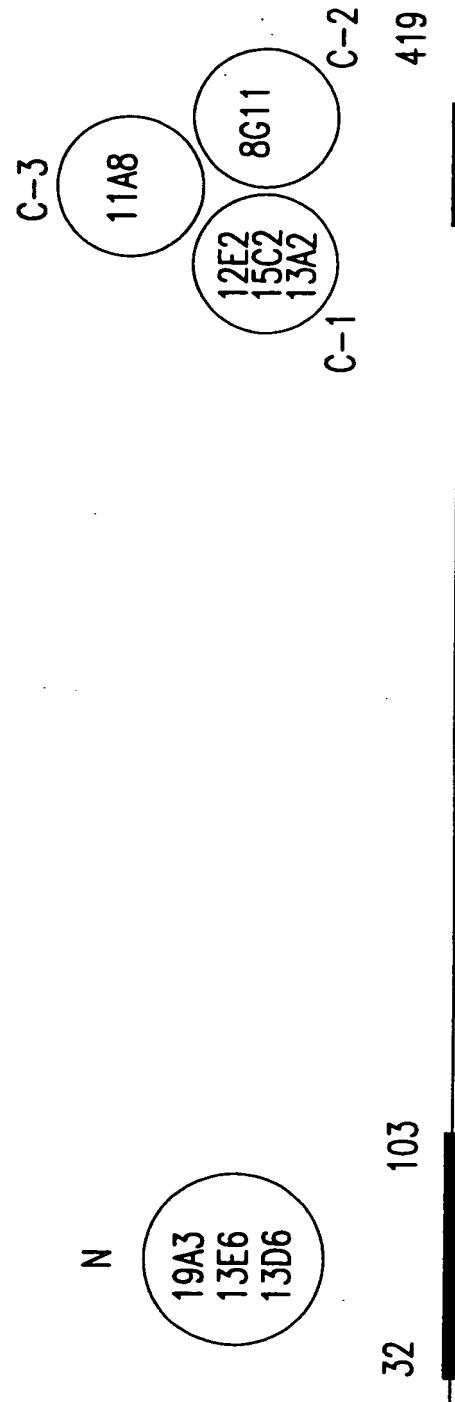


FIG.24



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MURINE VEGF-2 MAB STATUS

| | ISOTYPE | REL. AFFINITY
ng/ml | SPECIFICITY | WESTERN
ELISA | REACTIVITY | PURIFIED
mg |
|------|------------|------------------------|-------------|------------------|------------|----------------|
| 12E2 | $\gamma 1$ | <1 | C-1 | + | + | 27 |
| 13A2 | $\gamma 1$ | <1 | C-1 | n.t. | + | 27 |
| 15C2 | $\gamma 1$ | <1 | C-1 | n.t. | + | 10 |
| 13D6 | $\gamma 1$ | <1 | N | + | + | 25 |
| 13E6 | $\gamma 1$ | 1 | N | + | + | 38 |
| 19A3 | $\gamma 1$ | 1 | N | + | + | 54 |
| 8G11 | $\gamma 1$ | 5 | C-2 | + | + | 7 |
| 11A8 | $\gamma 1$ | <1 | C-3 | + | + | 9 |

FIG.25